

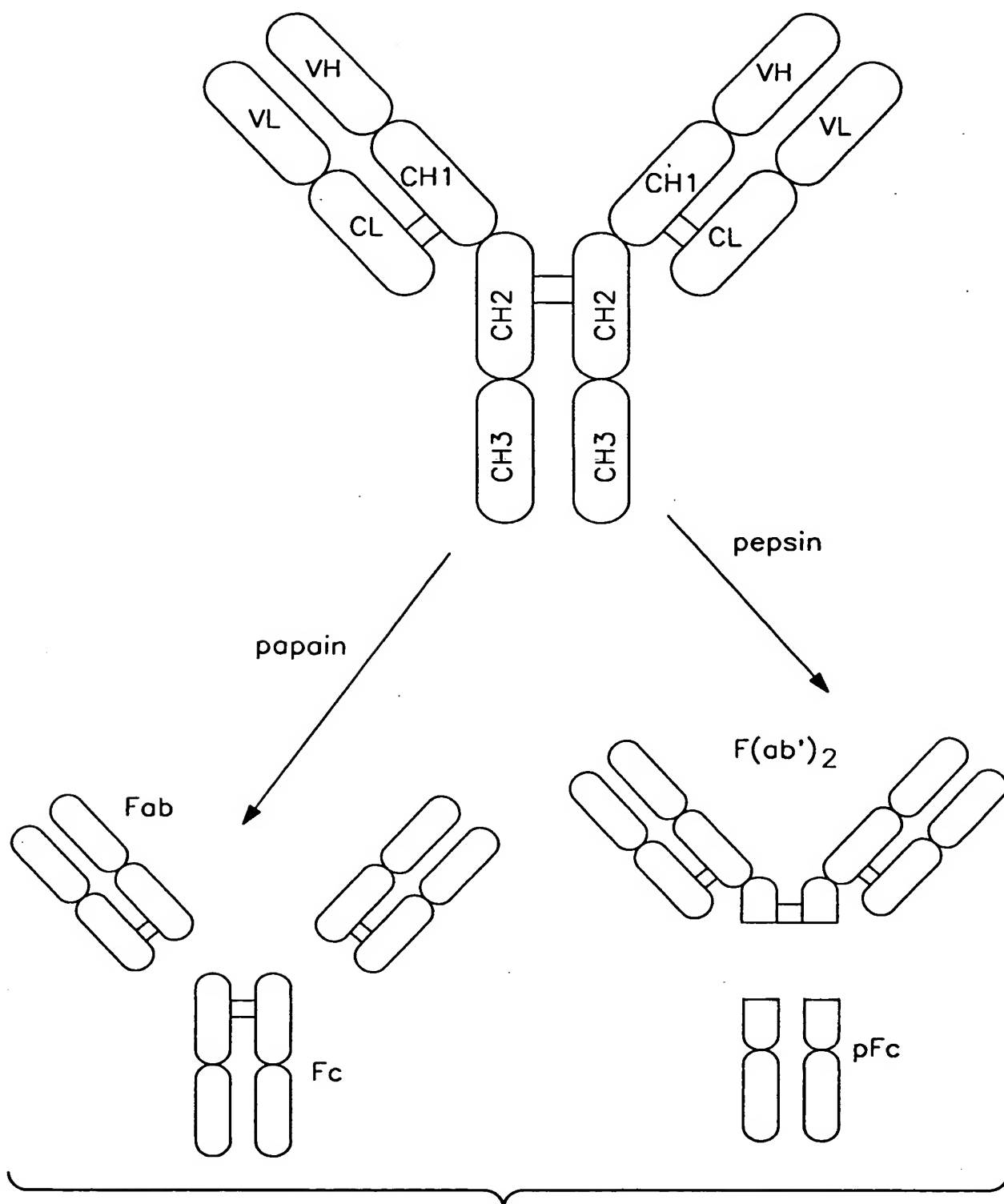
POLYPEPTIDE VARIANTS WITH ALTERED  
EFFECTOR FUNCTION

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**FIG.\_1**

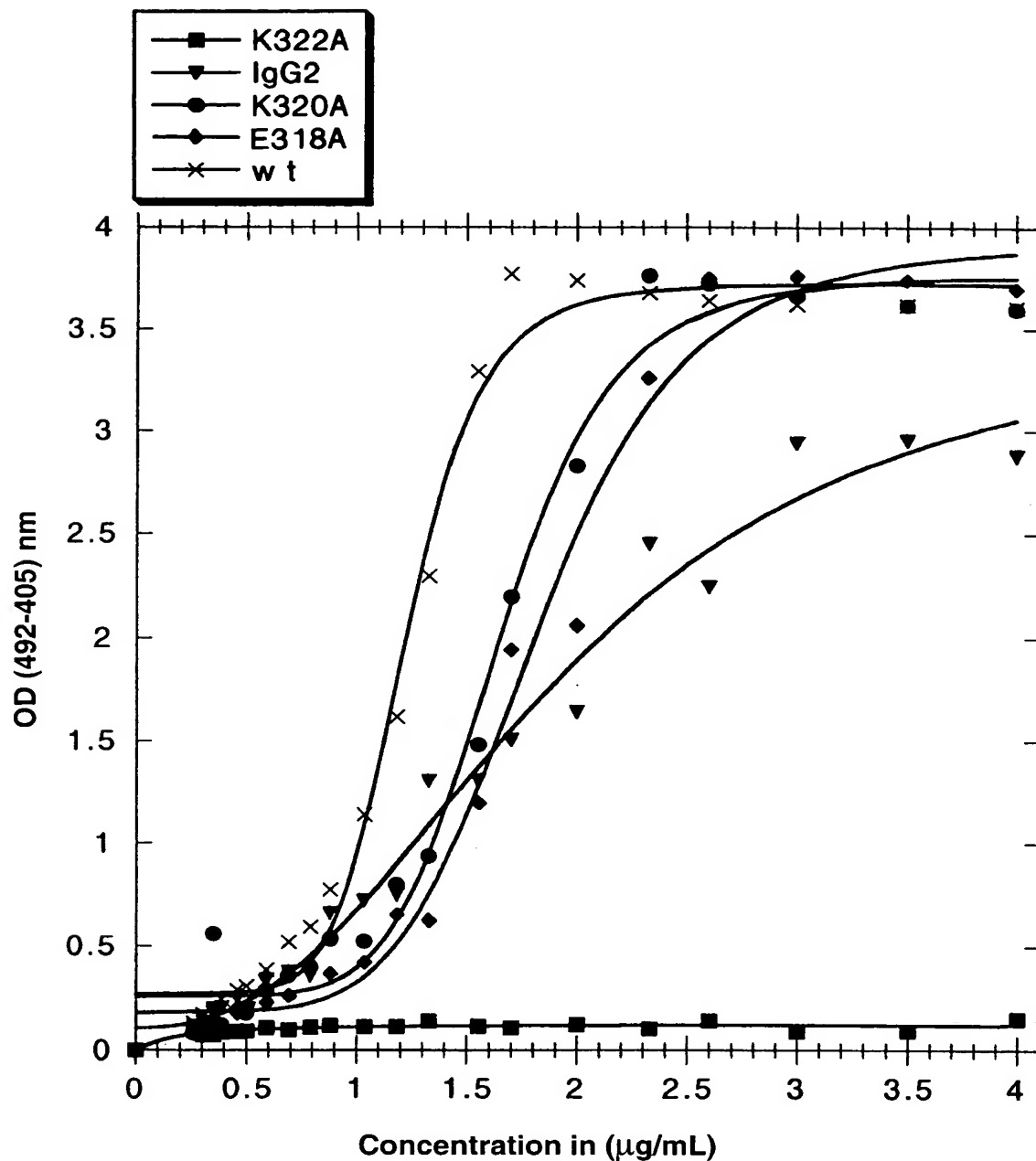
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**FIG. 2**

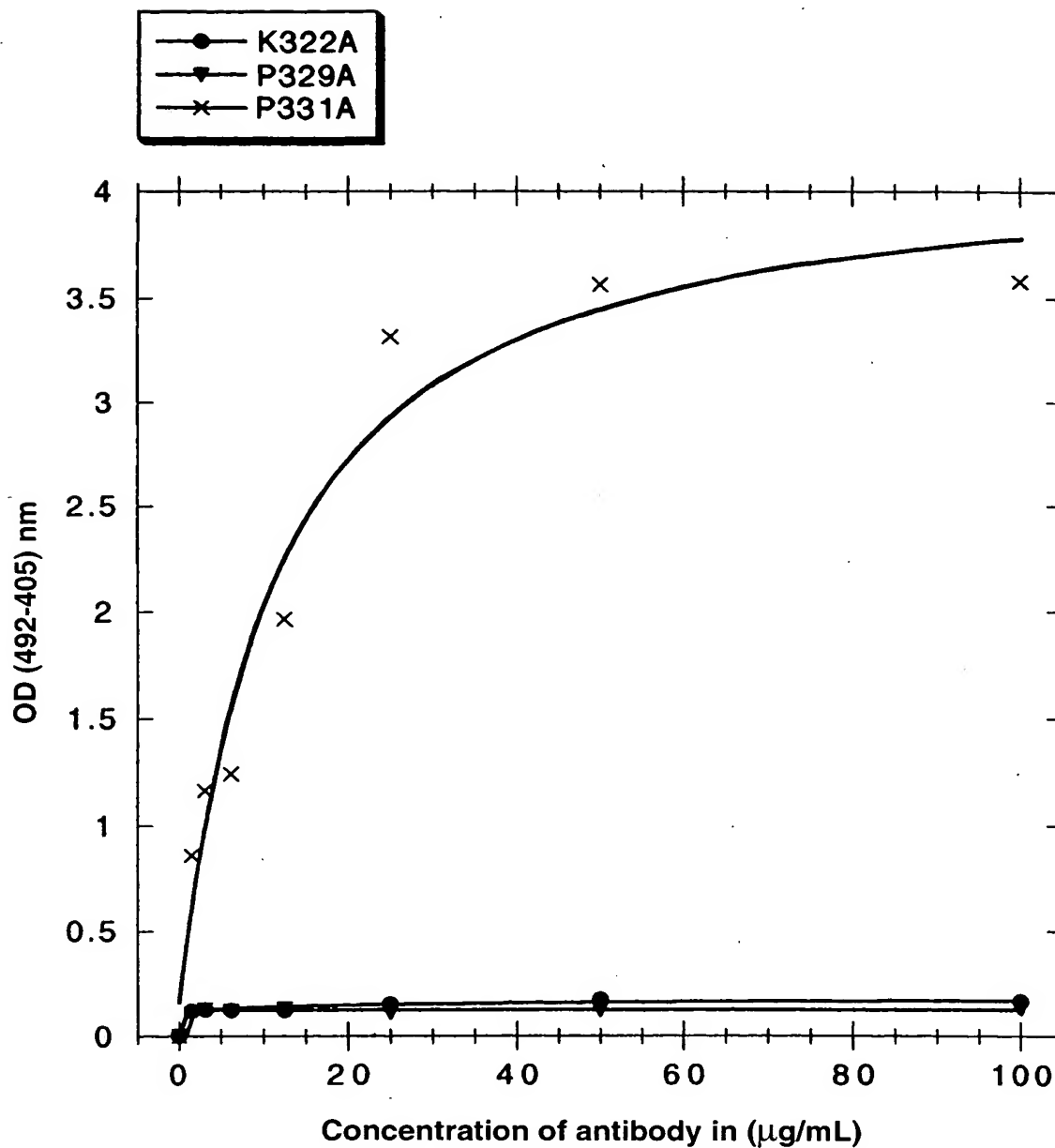
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**FIG. 3**

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(E27) - Light Chain

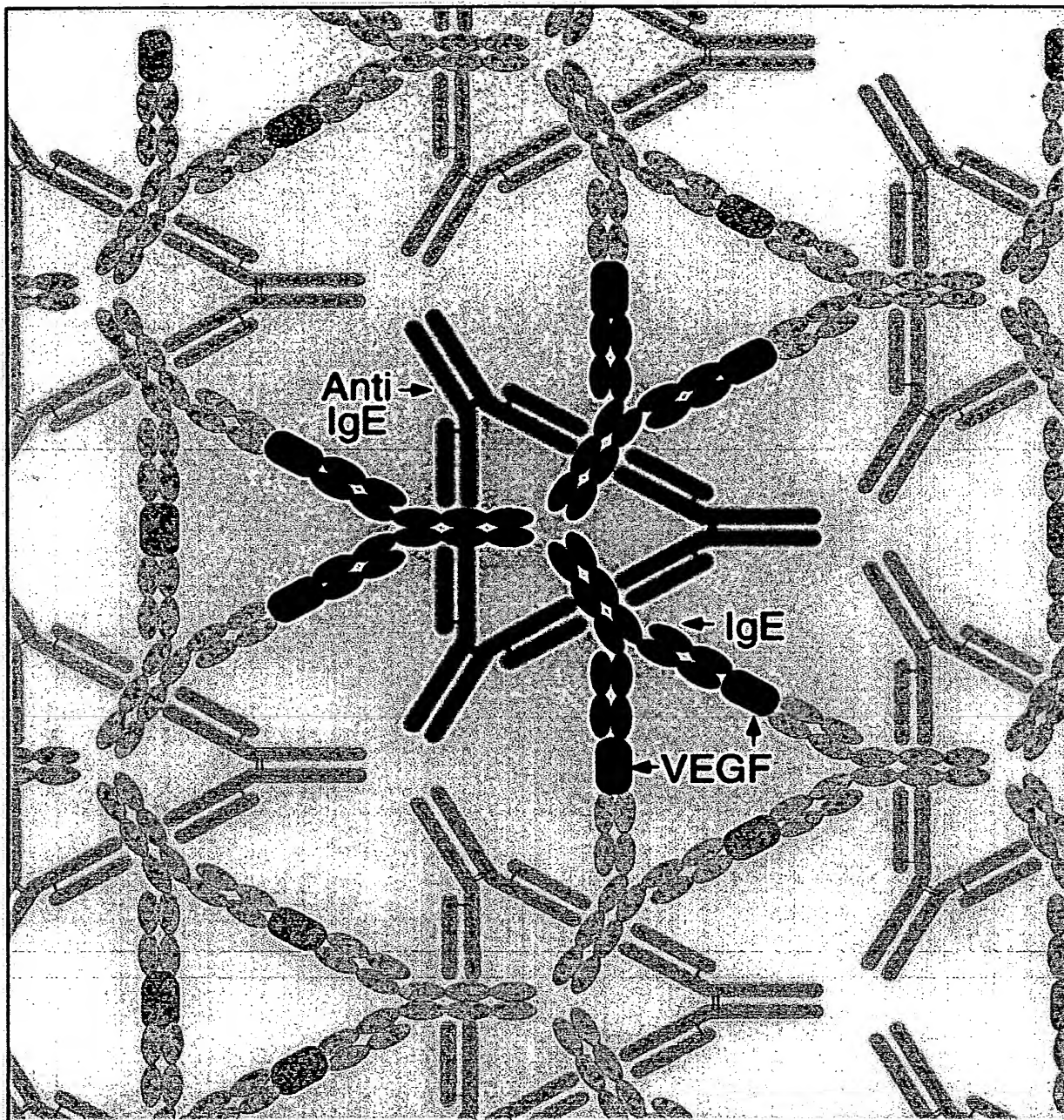
DIQLTQSPSS LSASVGDRVT ITCRASKPVD GEGDSYMNWY QQKPGKAPKL LIYAASYLES GVPSRFSGSG  
SGTDFTLTIS SLQPEDFATY YCQQSHEDPY TFGQGTKVEI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL  
NNFYBREAKV QWKVDNALQS GNSQESVTEQ DSKDSTYSLS STLTLKADY EKHKVYACEV THQGLSSPVT  
KSFNRGEC

**FIG.\_4A**

(E27) - Heavy Chain

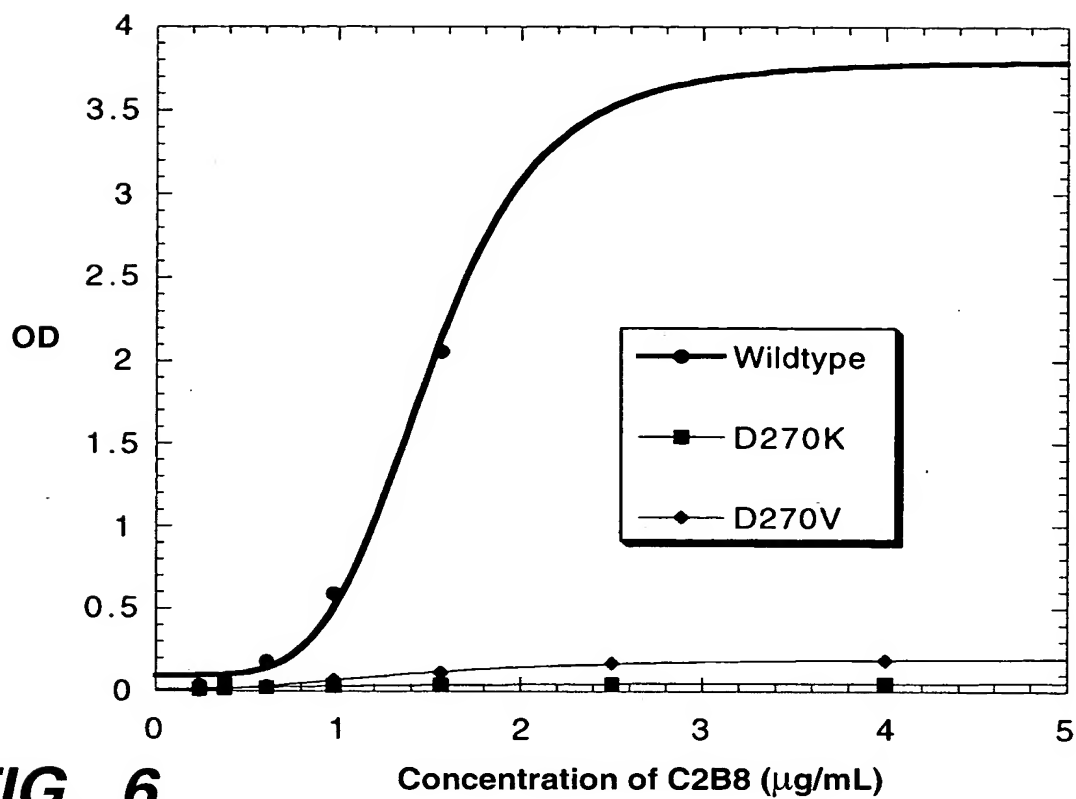
EVQLVESGGG LVQPGGSLRL SCAVSGYSIT SGYSWNWIRQ APGKGLEWVA SIKYSGETKY NPSVKGRITI  
SRDDSKNTFY LQMNSLRAED TAVYYCARGS HYFGHWHFV WGQGLVTVS SASTKGPSVF FLAPSSKSTS  
GGTAALGCLV KDYFPEPTV SWNSGALTSG VHTFPAVLQS SGLYSLSSV TVPSSSLGTQ TYICNVNKKP  
SNTKVDKKVE PKSCDKHTC PPCPAPELLG GPSVFLFPPK PKDTLMISRT PEVTCVVVDV SHEDPEVKFN  
WYVDGVEVHN AKTKPREEQY NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGPREP  
QVYTLPPSRE EMTKNQVSLT CLVKGFPYPSD IAVEWESNGQ PENNYKTTTP VLDSDGSFFL YSKLTVDKSR  
WQQGNVFCS VMHEALHNHY TQKSLSLSPG K

**FIG.\_4B**

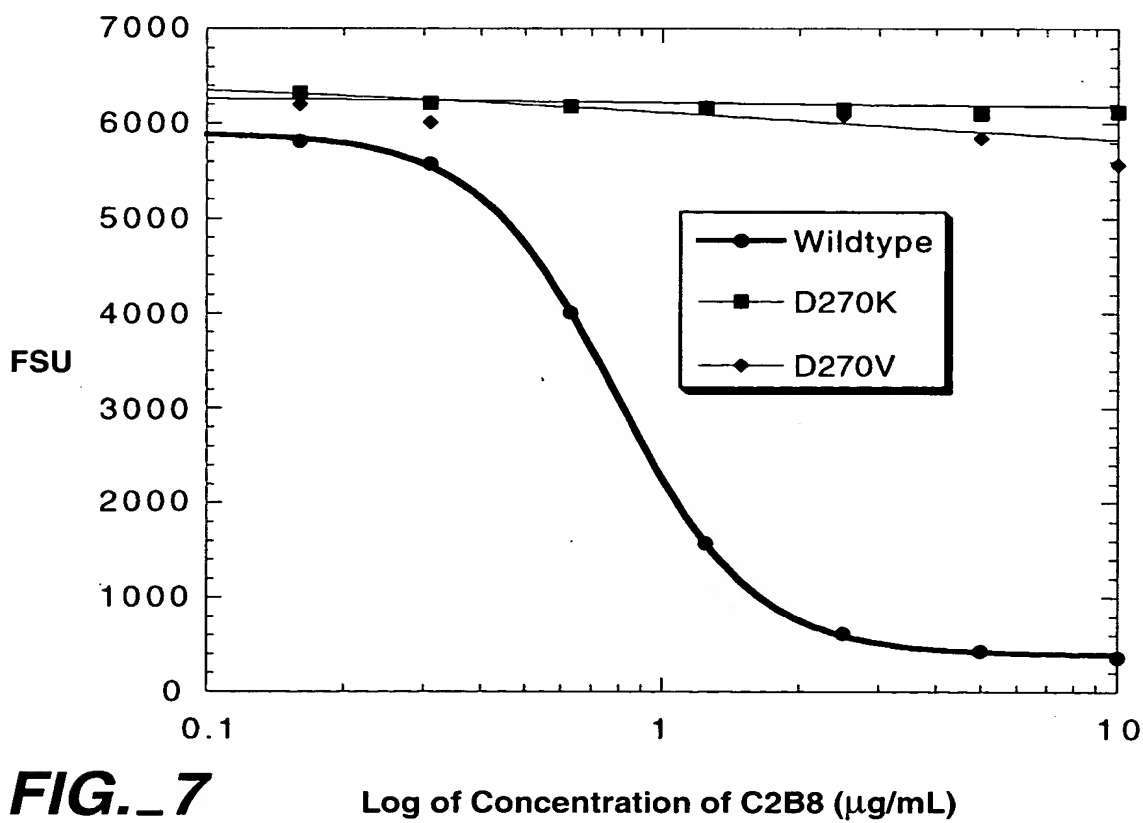


**FIG. 5**

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**FIG. 6**



**FIG. 7**

Log of Concentration of C2B8 ( $\mu\text{g/mL}$ )

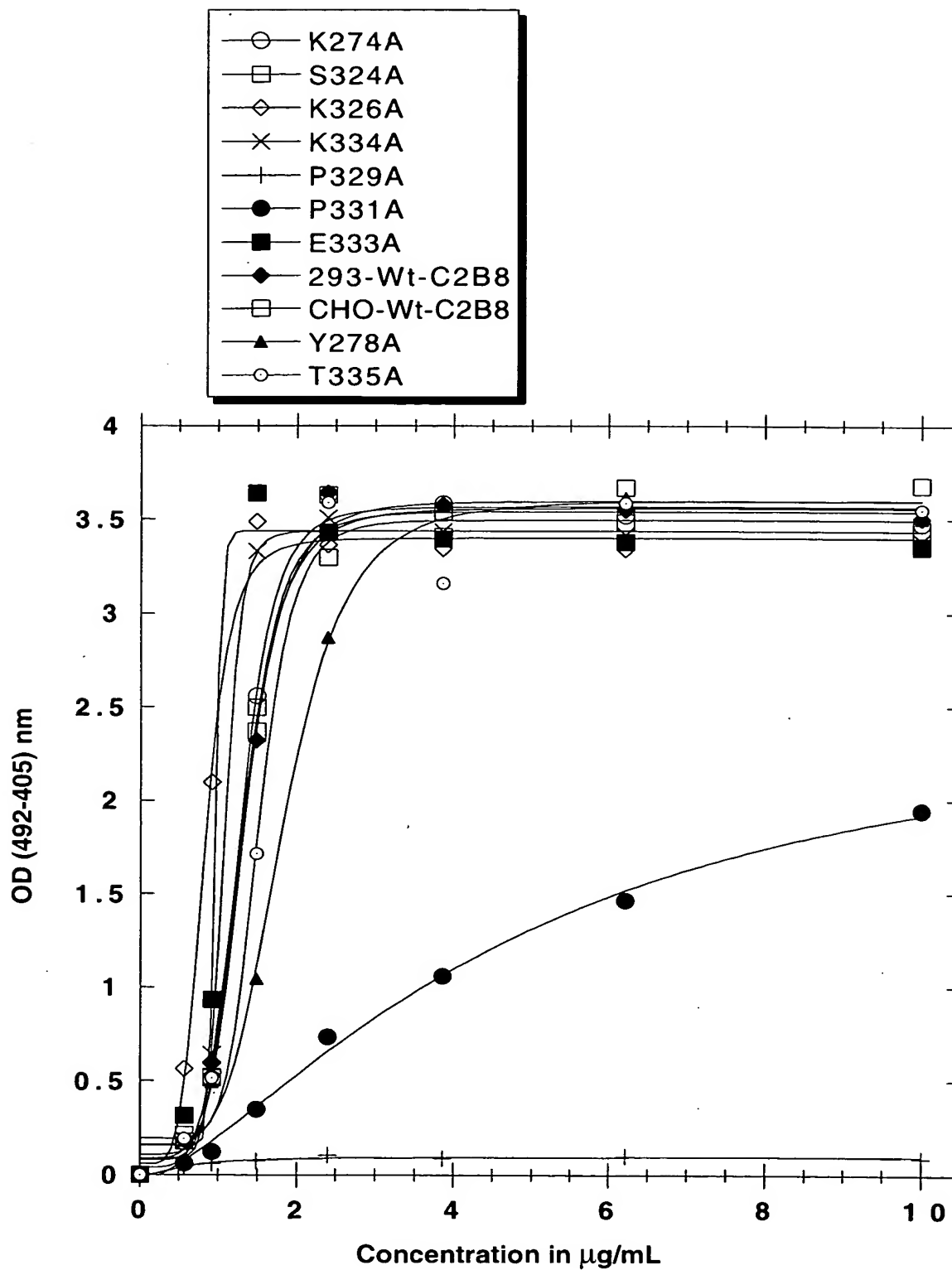
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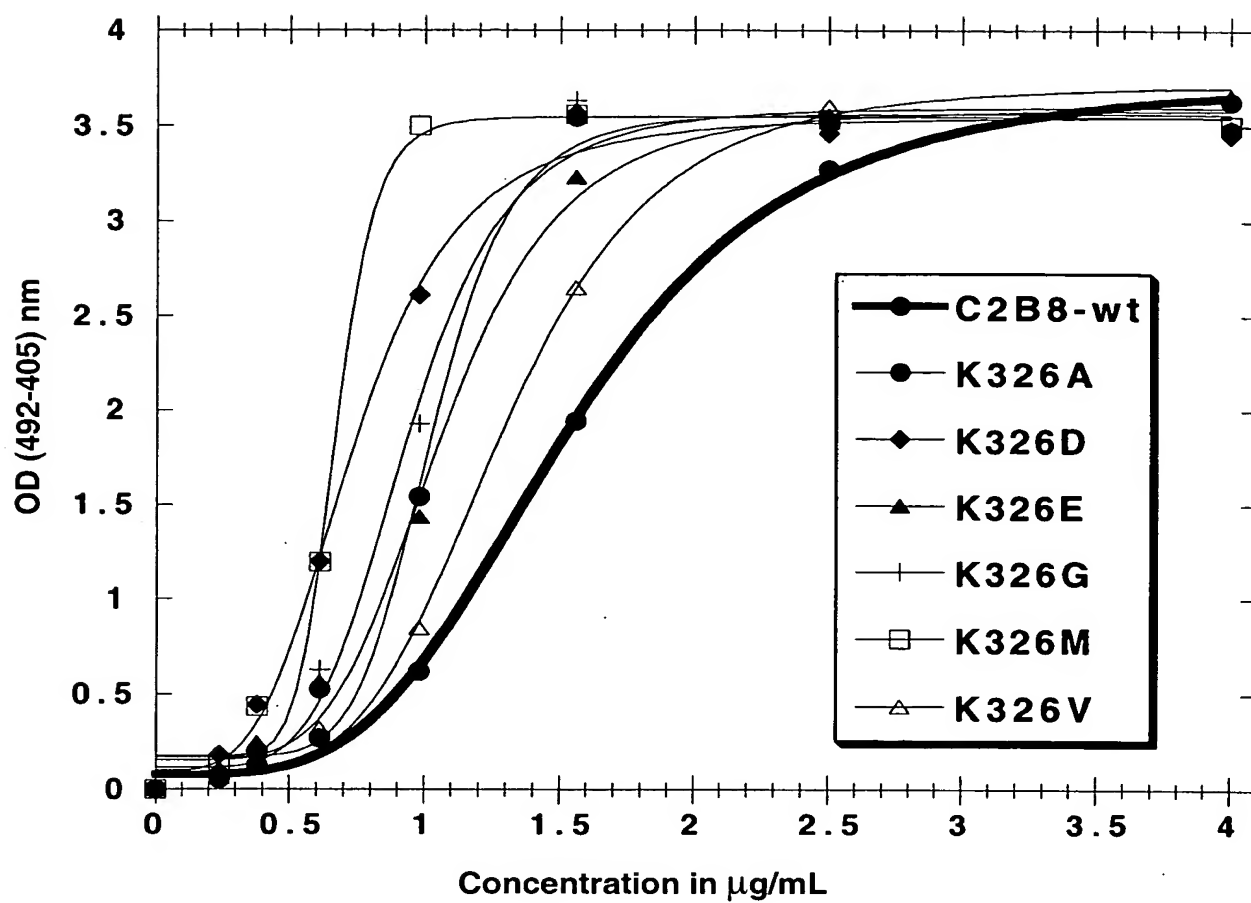
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**FIG.\_8**

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**FIG.\_9**



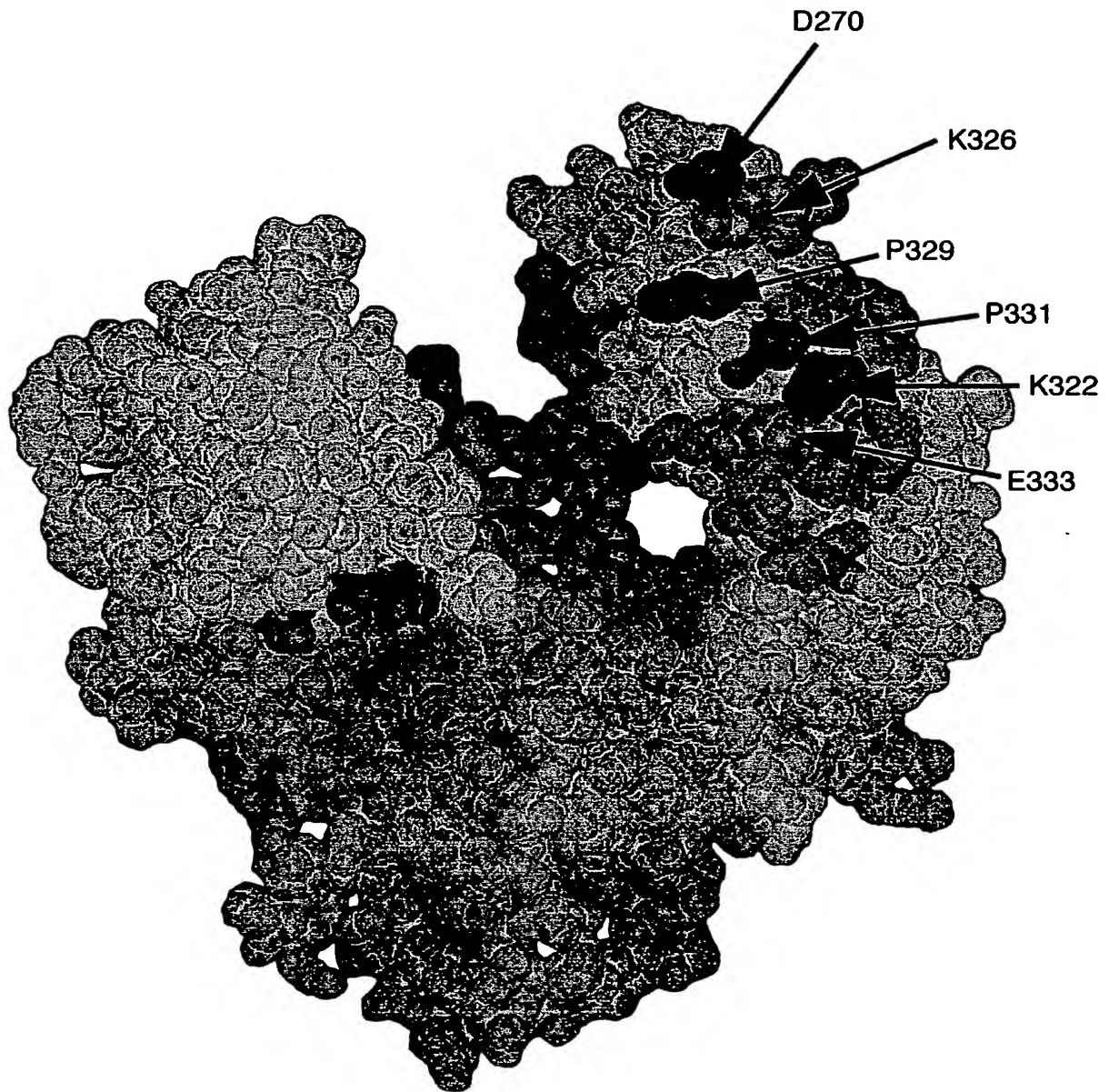
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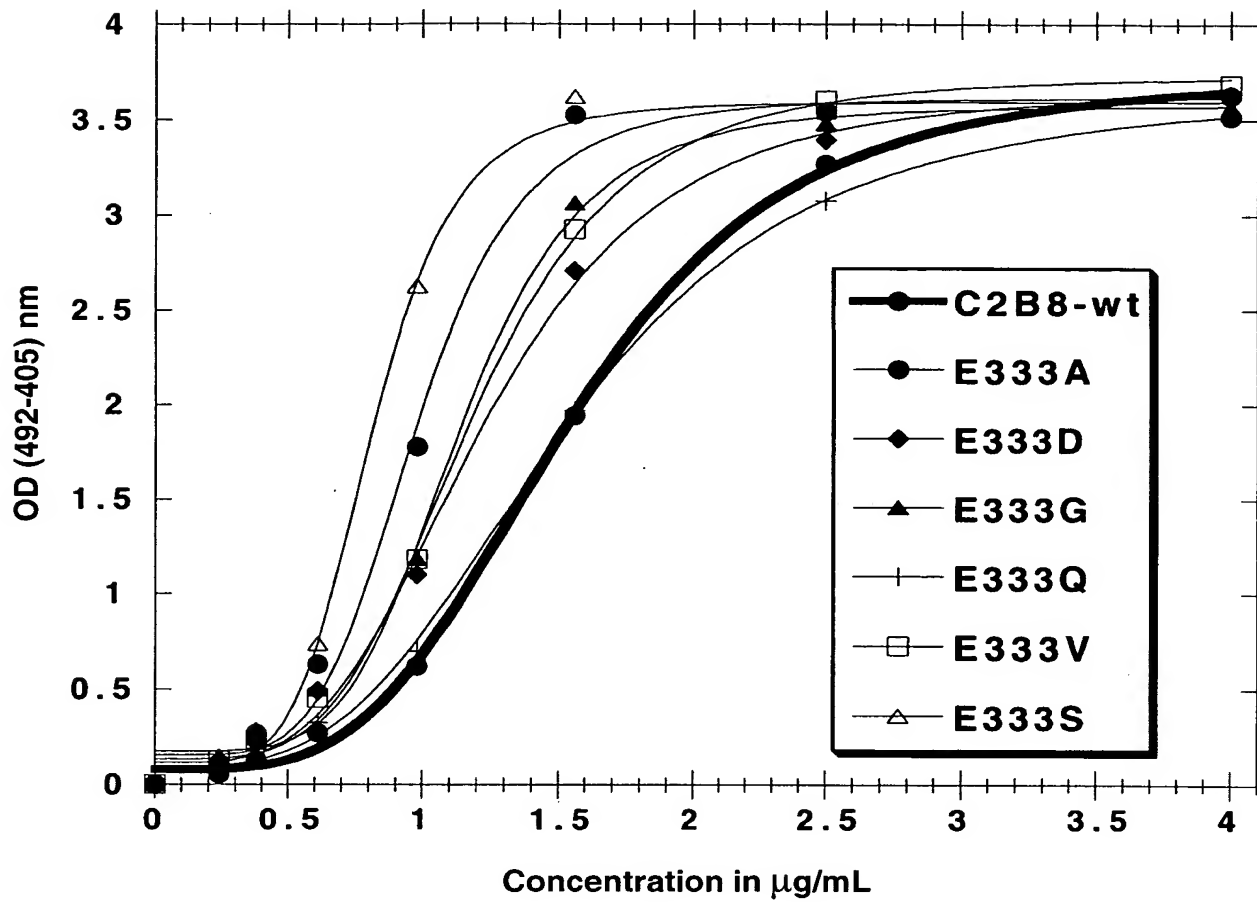
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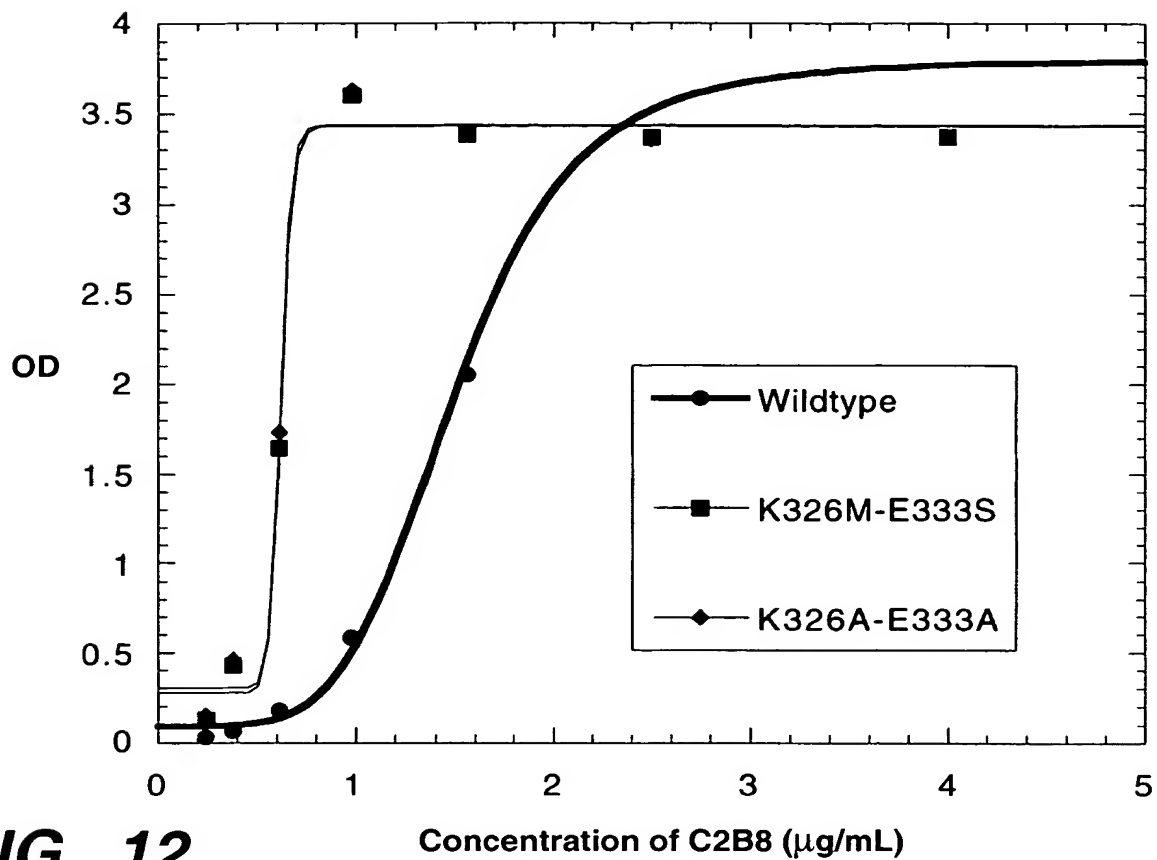
**FIG. 10**

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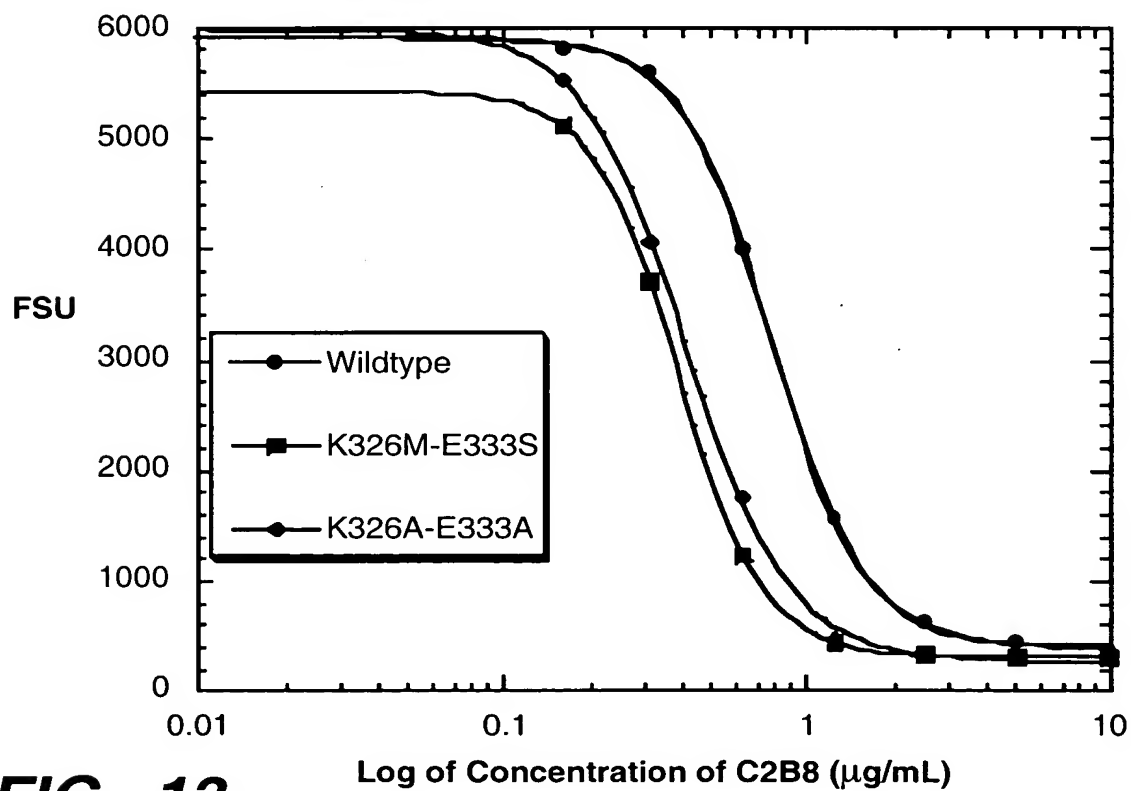


**FIG.\_11**

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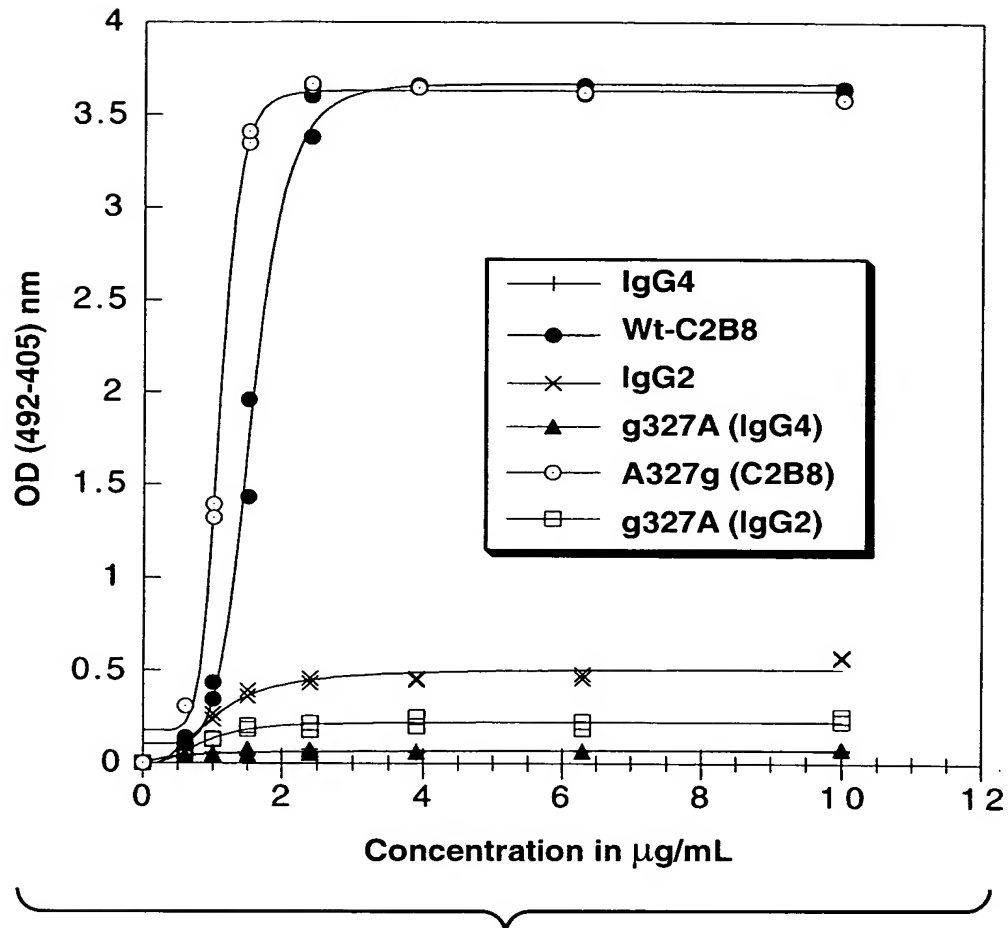
**FIG. 12**



**FIG. 13**

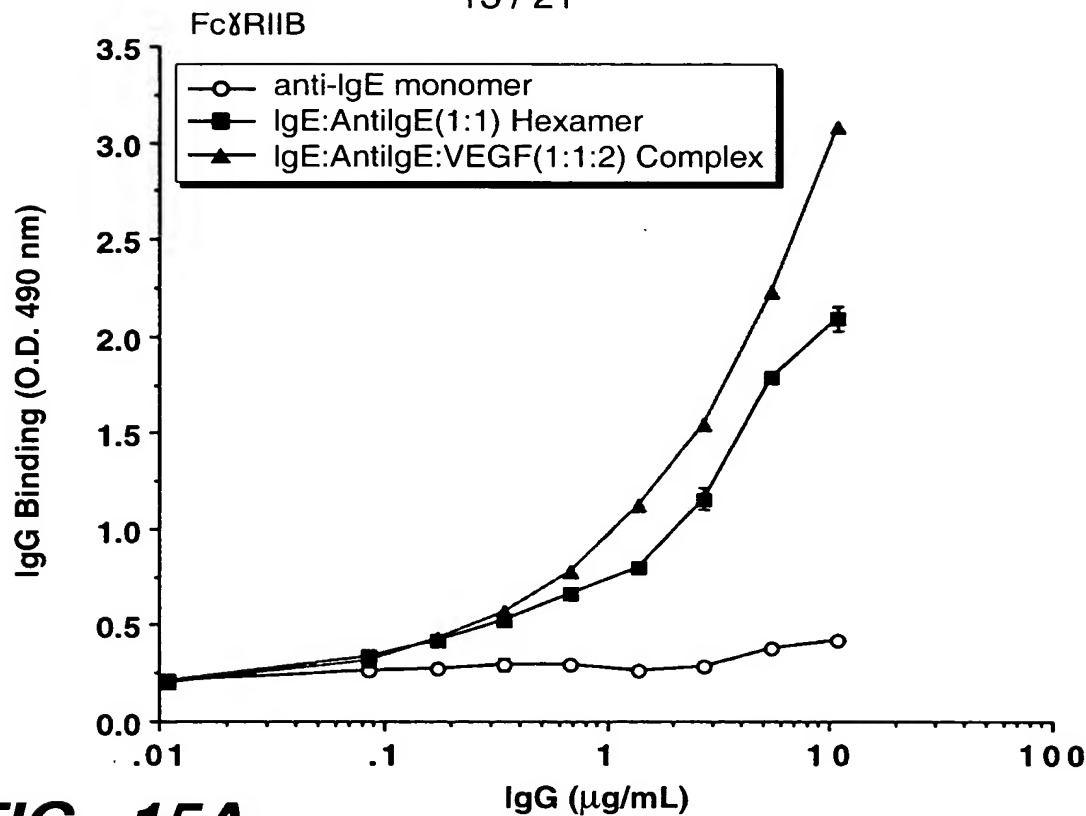
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EC50 of wt-C2B8 = 1.54  
EC50 of A327g (C2B8) = 1.08

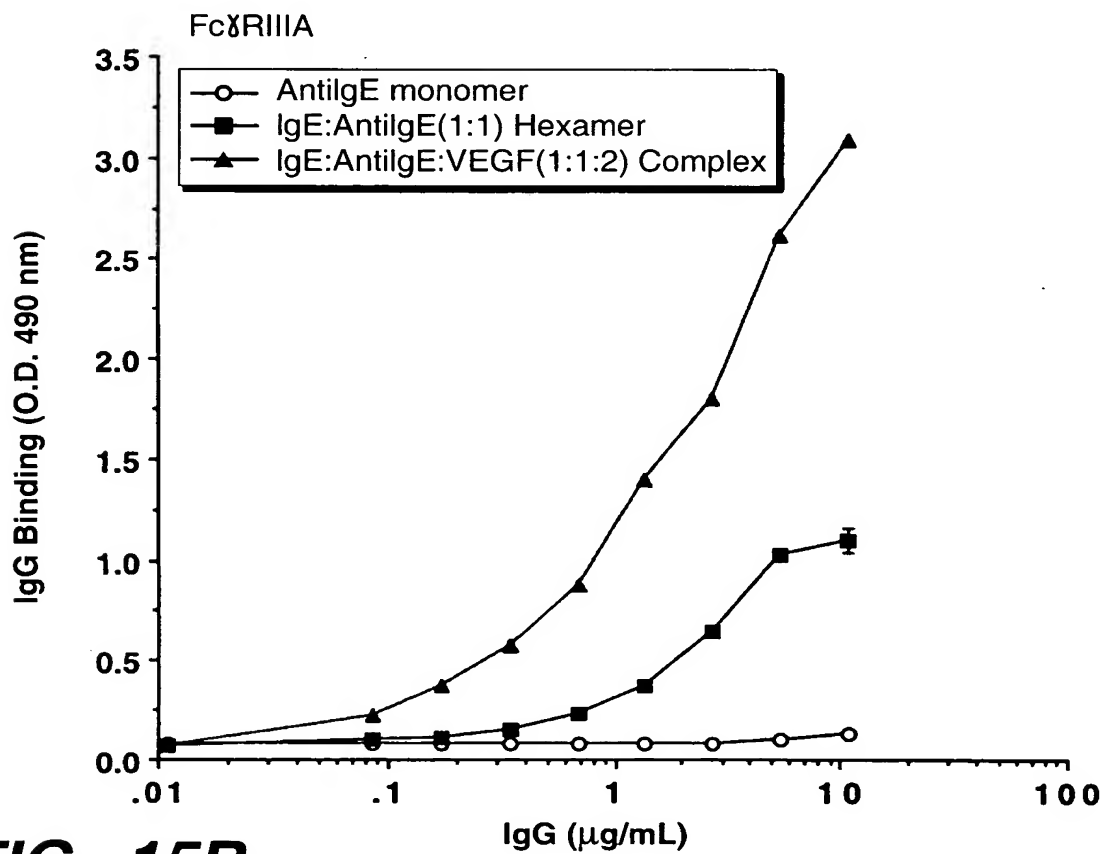


**FIG.\_14**

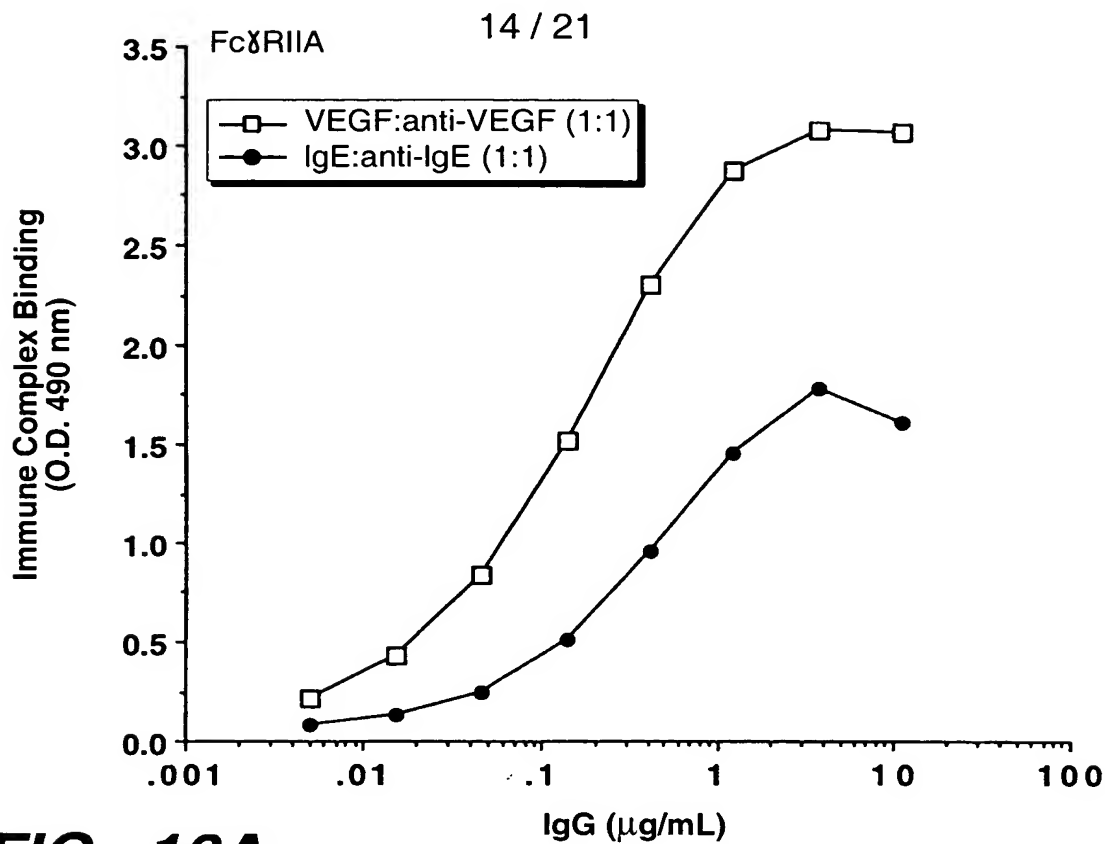
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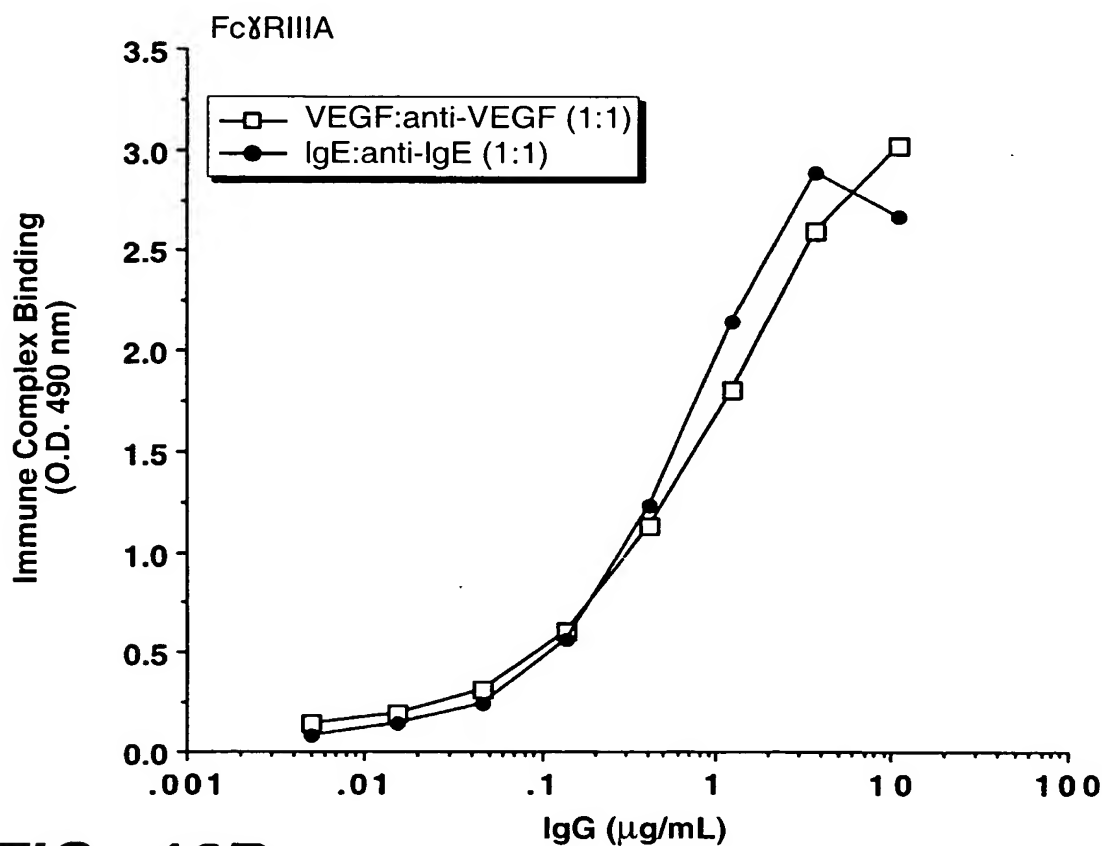
**FIG. 15A**



**FIG. 15B**

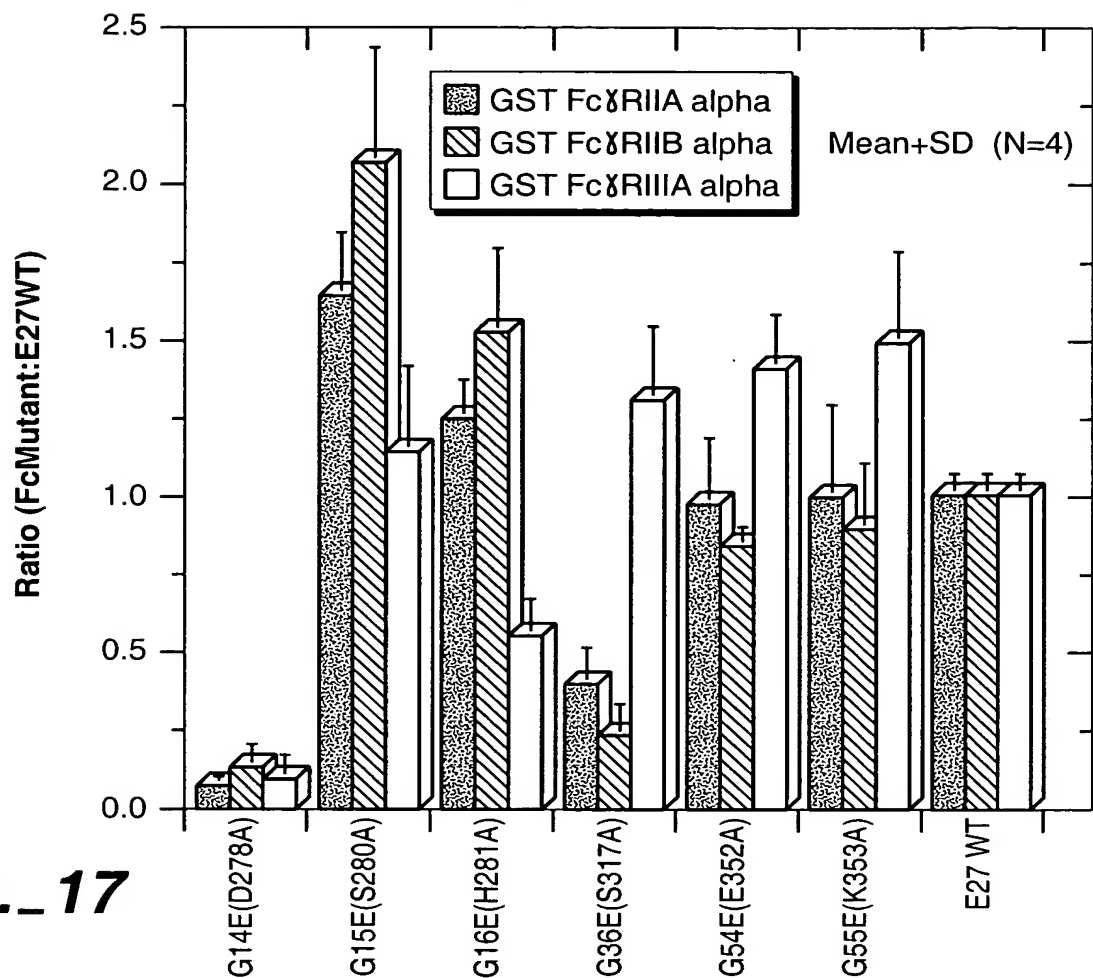


**FIG. 16A**

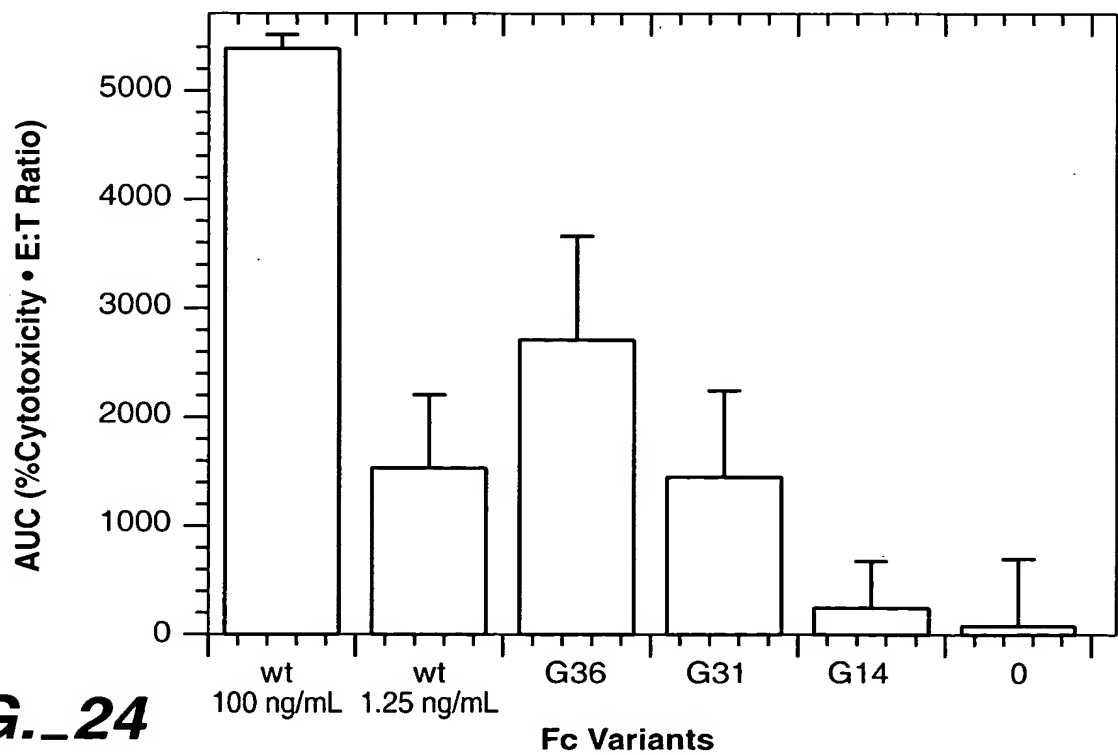


**FIG. 16B**

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**FIG. 17**



**FIG. 24**

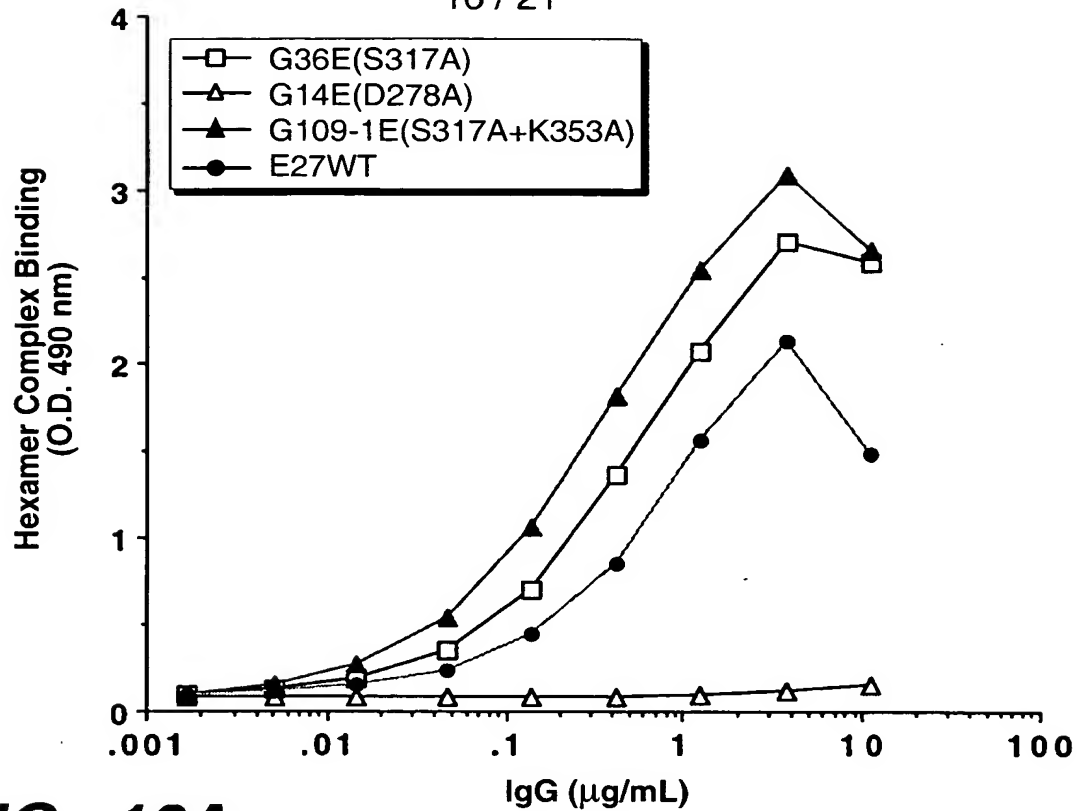
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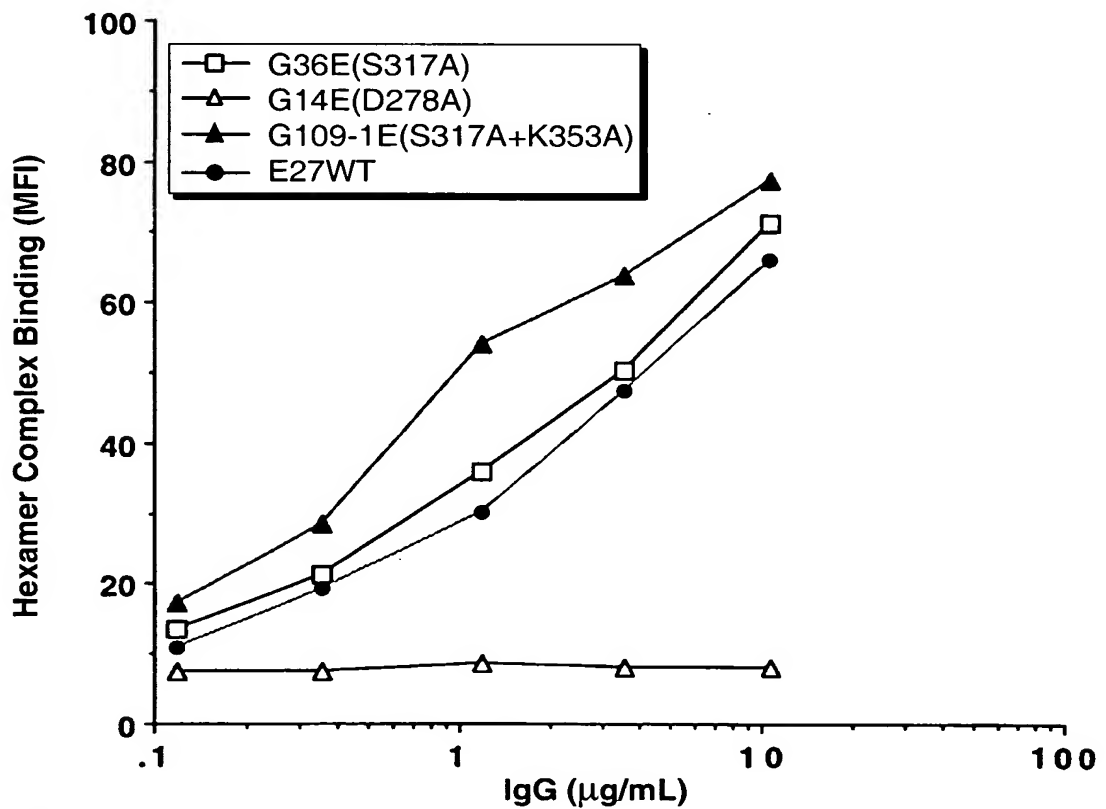
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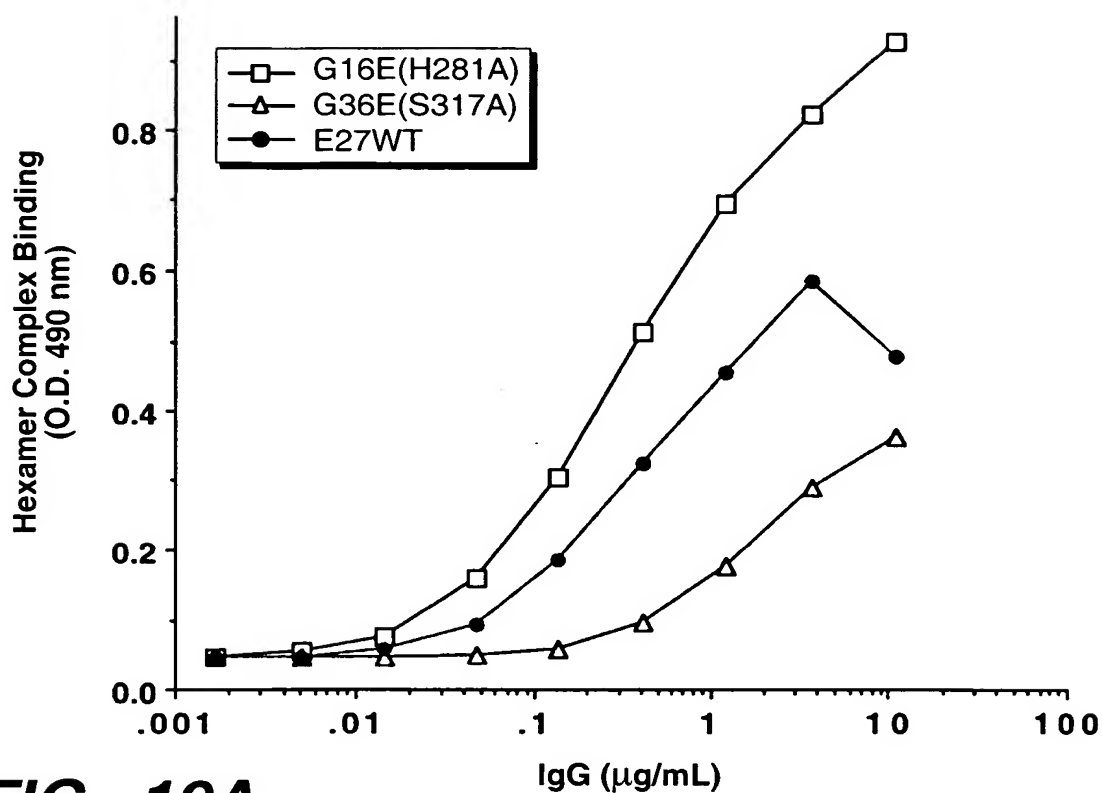
**FIG.\_18A**



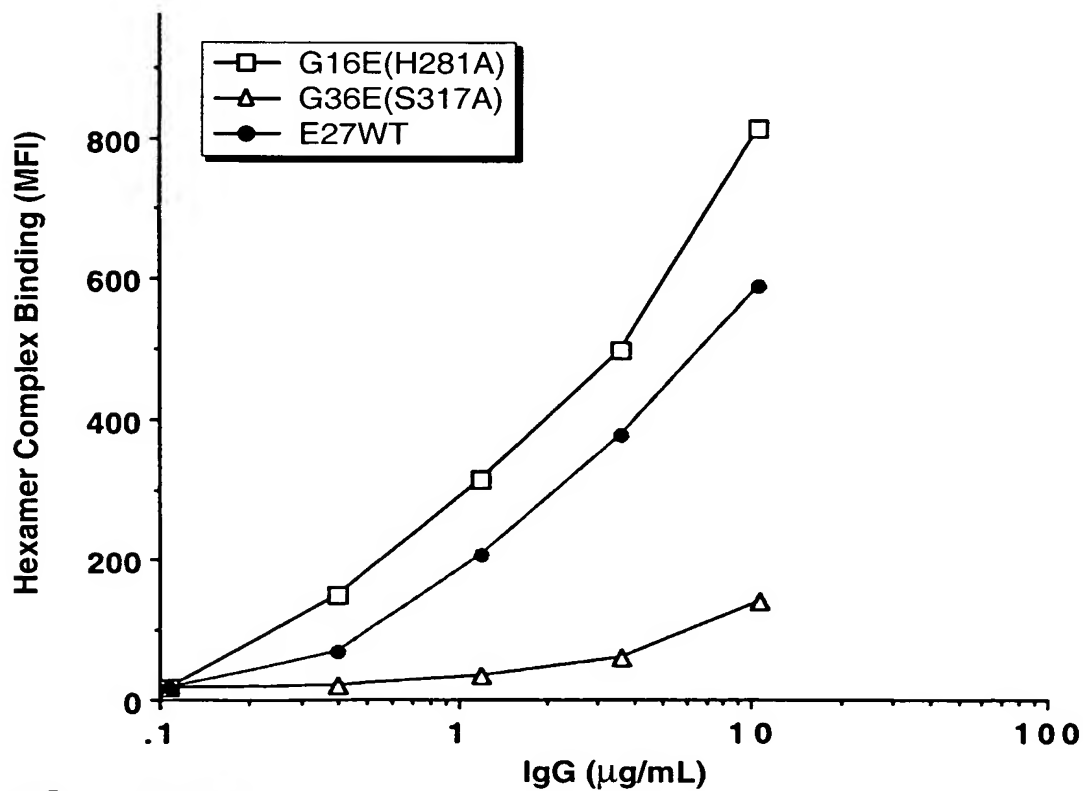
**FIG.\_18B**



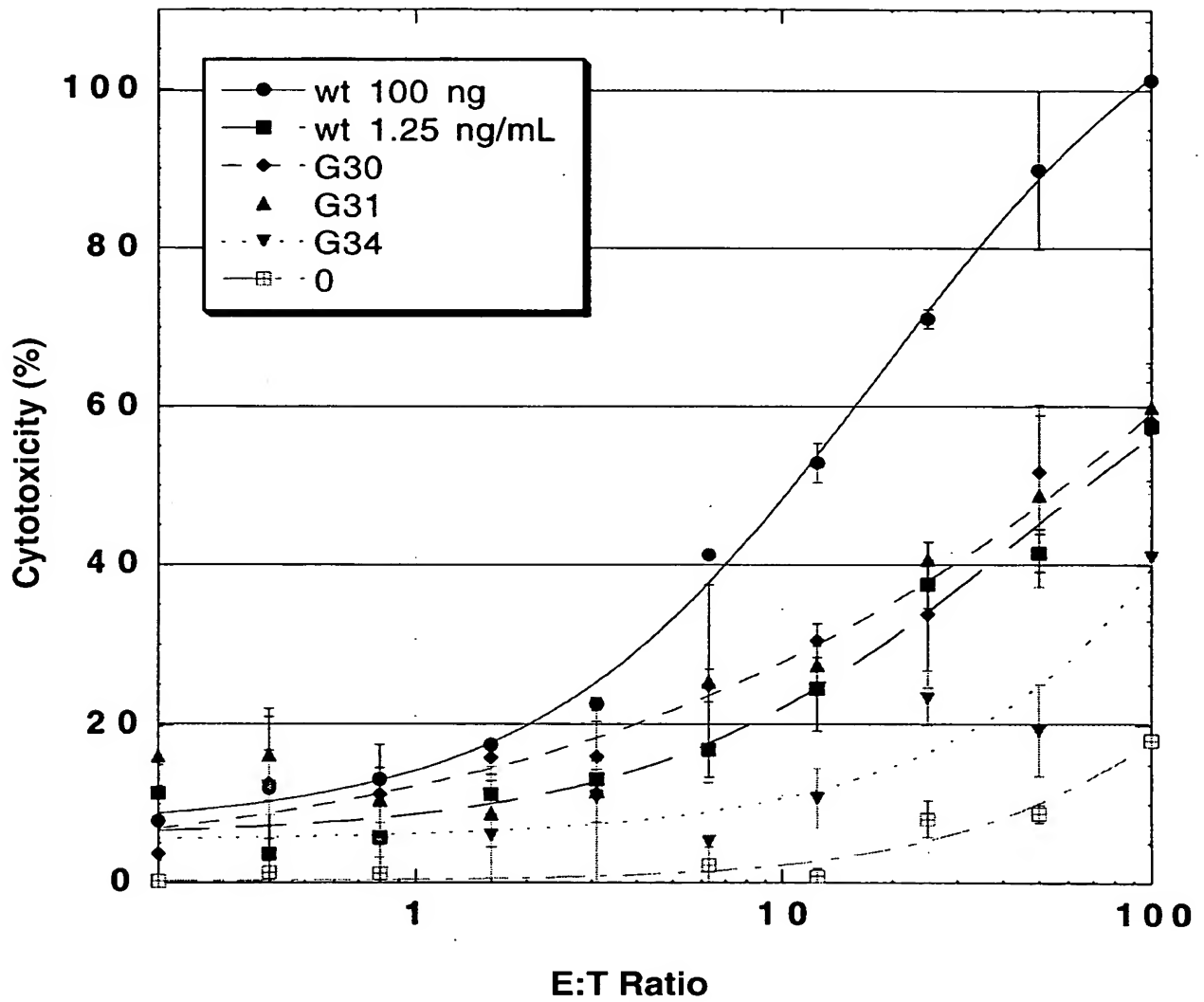
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**FIG. 19A**

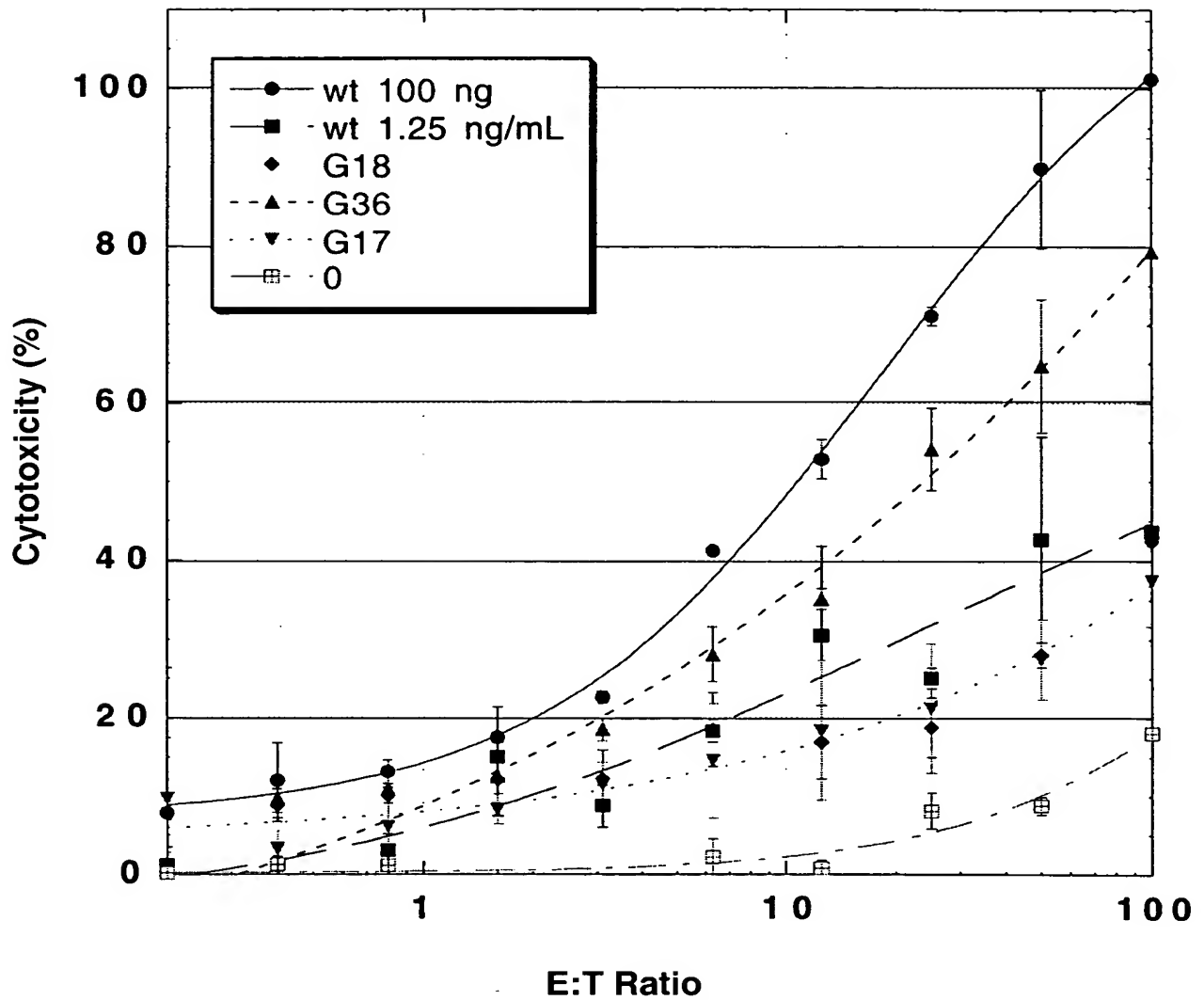


**FIG. 19B**



**FIG.\_20**

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**FIG. 21**

POLYPEPTIDE VARIANTS WITH ALTERED  
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	230	240	250	260	270
humIgG1	PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV				
humIgG2	PAP - PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYV				
humIgG3	PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYV				
humIgG4	PAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSEQEDPEVQFNWYV				
murIgG1	---TVPEVSSVFIFPPKPKDVLTLTPKVTCTVVVDISKDDPEVQFSWFV				
murIgG2A	PAPNLLGGPSVFIFPPKIKDVLMLISLPIVTCVVVDVSEDDPDVQISWFV				
murIgG2B	PAPNLEGGPSVFIFPPNIKDVLMLISLTPKVTCTVVVDVSEDDPDVQISWFV				
murIgG3	PPGNILGGPSVFIFPPKPKDALMISLTPKVTCTVVVDVSEDDPDVHVSWFV				
	280	290	300	310	320
humIgG1	DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP				
humIgG2	DGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLP				
humIgG3	DGVEVHNAKTKPREEQFNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALP				
humIgG4	DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP				
murIgG1	DDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDCLNGKEFKCRVNSAAFP				
murIgG2A	NNVEVHTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLP				
murIgG2B	NNVEVHTAQTQTHREDYNSTIRVVSHPPIQHQDWMSGKEFKCKVNNKDLP				
murIgG3	DNKEVHTAWTQPREAQYNSTFRVVSALPIQHQDWMRGKEFKCKVNNKALP				
	330	340	350	360	370
humIgG1	APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV D L				
humIgG2	APIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV				
humIgG3	APIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV				
humIgG4	SSEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAV				
murIgG1	APIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCLMITDFFPEDITV				
murIgG2A	APIERTISKPKGSVRAPQVYVLPPEEEMTKKQVTLTCMVTDFMPEDIYV				
murIgG2B	SPIERTISKPKGLVRAPQVYTLPPPAEQLSRKDVSLTCLVVGFNPGDISV				
murIgG3	APIERTISKPKGRAQTPQVYTIPPPREQMSKKKVSLTCLVTNFFSEAISV				
	380	390	400	410	420
humIgG1	EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH				
humIgG2	EWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH				
humIgG3	EWESSGQPENNYNTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMH				
humIgG4	EWZSNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMH				
murIgG1	EQWNGQPAENYKNTQPIMDTDGSYFVYSKLNQKSNWEAGNTFTCSVLH				
murIgG2A	EWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVVH				
murIgG2B	EWTNNGHTEENYKDTAPVLDSDGSYFIYSKLNMKTSKWEKTDSEFCNVRH				
murIgG3	EWERNGELEQDYKNTPPILSDSGTYFLYSKLTVDTDVSWLQGEIFTCSVVH				
	430	440			
humIgG1	EALHNHYTQKSLSLSPGK				
humIgG2	EALHNHYTQKSLSLSPGK				
humIgG3	EALHNRFTQKSLSLSPGK				
humIgG4	EALHNHYTQKSLSLSPGK				
murIgG1	EGLHNHHTTKSLSHSPGK				
murIgG2A	EGLHNHHTTKSFSRTPGK				
murIgG2B	EGLKNYYLKKKTISRSPGK				
murIgG3	EALHNHHTQKNLSRSPGK				

**FIG. 22A**

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## Percent Identity Among Fc Sequences

	1	2	3	4	5	6	7	8
1. humIgG1	-	94	94	94	64	66	63	68
2. humIgG2		-	93	92	65	63	60	67
3. humIgG3			-	91	64	64	61	67
4. humIgG4				-	62	64	61	64
5. murIgG1					-	65	61	67
6. murIgG2A						-	77	70
7. murIgG2B							-	68
8. murIgG3								-

**FIG.\_22B**

	230	240	250	260	270
humIgG1	PAP	ELLGGPSVFLFPPKPKD	TL	MISRTPEVTCVVVDV	SHEDPEVKFNWYV
humIgG2	PAP	-PVAGPSVFLFPPKPKD	TL	MISRTPEVTCVVVDV	SHEDPEVQFNWYV
humIgG3	PAP	ELLGGPSVFLFPPKPKD	TL	MISRTPEVTCVVVDV	SHEDPEVQFKWYV
humIgG4	PAPE	FLGGPSVFLFPPKPKD	TL	MISRTPEVTCVVVDV	SQEDPEVQFNWYV
	***				* * *
	280	290	300	310	320
humIgG1	DGVEVHNAKTKPREEQ	YNSTYRVVSVLTVLHQD	WLNGKEYKCKVSNKALP		
humIgG2	DGVEVHNAKTKPREEQ	FNSTFRVSVLTVVHQD	WLNGKEYKCKVSNKGLP		
humIgG3	DGVEVHNAKTKPREEQ	FNSTFRVSVLTVLHQD	WLNGKEYKCKVSNKALP		
humIgG4	DGVEVHNAKTKPREEQ	FNSTYRVVSVLTVLHQD	WLNGKEYKCKVSNKGLP		
		*	*	*	*
	330	340	350	360	370
humIgG1	APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV				
				D L	
humIgG2	APIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV				
humIgG3	APIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV				
humIgG4	SSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAV				
	**	*		*	
	380	390	400	410	420
humIgG1	EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV	FSCSVMH			
humIgG2	EWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNV	FSCSVMH			
humIgG3	EWESSGQPENNYNTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIF	FSCSVMH			
humIgG4	EWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNV	FSCSVMH			
	*	*	*	*	* *
	430	440			
humIgG1	EALHNHYTQKSLSLSPGK				
humIgG2	EALHNHYTQKSLSLSPGK				
humIgG3	EALHNRFTQKSLSLSPGK				
humIgG4	EALHNHYTQKSLSLSLGK				
	**	*			

**FIG.\_23**